



FIG. 1.

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CLUSTAL W (1.7) multiple sequence alignment

```

P93621      MGLCKILSISSFLLTTLFFTSYAATFNIQNHCSYTVWAAAVP-GGGMQLGSGQSWSLNV
Q04708      MRFTTTLPIILIPLLLSLLFTSTHAATFDILNKCTYTVWAAASP-GGGRRLDSGQSWTITV
P25096      -----ARFEITNRCTYTVWAAASVPVGGGVQLNPGQSWSDV
PR5-1sun    ---MTTSTLPTFLLLAILFHYTNAAVFTIRNNCPYTVWAGAVP-GGGRQLNSGQTWSLTV
Q01591      -----FFLLAFVITYYAATFEVRNNCPYTVWAASTPIGGGRRLDRGQTVVINA
P50701      ---MAYLRSSFVFFLLAFVITYYAATIEVRNNCPYTVWAASTPIGGGRRLDRGQTVVINA
                                * : : *.*.*****. : * *** :*. **: * : .
  
```

```

P93621      NAGTTGARVWGRTNCFDASGNGKCETGDCGGLLQCTAYGTPPNTLAEFALNQFSNLDFF
Q04708      NPGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPNTLAEFALNQPNLDYI
P25096      PAGTKGARVWARTGCNFDGSGRGGCQTGDCGGVLQCKAYGAPPNTLAEYGLNGFNLDFF
PR5-1sun    AAGTAGARIWPRTNCFDGSGRGRCQTGDCNGLLQCCQNYGTPPNTLAEYALNQFNLDFF
Q01591      PRGTMARIWGRTNCFDGDGRGSCQTGDCGGVLQCTGWGKPPNTLAEYALDQFSNLDFF
P50701      PRGTMARIWGRTNCFDAGARGSCQTGDCGGVLQCTGWGKPPNTLAEYALDQFSNLDFF
                                ** **: * *.*.*. *. * *:*****. *: * :.***:
  
```

```

P93621      FDISLVDGFNVPMFNP--SNGCTRGISCTADIVGECPAALKTTGGCNPCTVFKTDEY
Q04708      IDISLVDGFNIPMDFS-----GC-RGIQCSVDINGQCPSELKAPGGCNPCTVFKTNEY
P25096      FDISLVDGFNVPMDFSPT--SNGCTRGISCTADINGQCPSELKTQGGCNPCTVFKTDQY
PR5-1sun    FDISLVDGFNVPMVFRPN--SNGCTRGISCTADINGQCPGELRAPGGCNPCTVYKTDQY
Q01591      WDISLVDGFNIPMTFAPTNPSSGKCHAIHCTANINGECPGSLRVPGGCNPCTTFGGQQY
P50701      WDISLVDGFNIPMTFAPTNPSSGKCHAIHCTANINGECPGSLRVPGGCNPCTTFGGQQY
                                *****: ** *      * : , * *: : * *: **, *: , *****: : : *
  
```

```

P93621      CCNSG--SCNATTYSEFFKTRCPDAYSYPKDDQTSTFTCPAG-TNYEVIFCP-----
Q04708      CCTDGPSCGPTTYSKFFKDRCPDAYSYPQDDKTSLFTCPSG-TNYKVTFCP-----
P25096      CCNSG--SCGPTDYSRFFKQRCPDAYSYPKDDPPSTFTCNGG-TDYRVVFCP-----
PR5-1sun    CCNSG--NCGPTDLRFFKTRCPDAYSYPKDDPTSTFTCPGG-TNYDVIFCP-----
Q01591      CCTQG--PCGPTDLRFFKQRCPDAYSYPQDDPTSTFTCPSGSTNYRVVFCPNGVTSPNF
P50701      CCTQG--PCGPTDLRFFKQRCPDAYSYPQDDPTSTFTCPSGSTNYRVVFCPNGVTSPNF
                                **, *  *, *  *, *** *****: **, * ****, * *: * * ***
  
```

```

P93621      -----
Q04708      -----
P25096      -----
PR5-1sun    -----
Q01591      PLEMPSSDEEAK
P50701      PLEMPASDEEAK
  
```

FIG. 2.

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CLUSTAL W (1.7) multiple sequence alignment

```

P30986  -MENKTIFFSLSIFLS-----LLNCALGG--ND--LLSCLTFNGVRNHTV---FSADS
P93479  MMCRSLTLRFFLFIVL-----LQTCVRGGDVNDNLLSSCLNSHGVHNFIT---LSTDT
Sunf-19 ---METSILTLLLLLS-----TQSSATSRSDTDR-FIQCLHADRADPSFPIITGEVYTPG
Sunf-15 ---MQTSILTLLLLLS-----TQSSATSRSDTDR-FIQCLHADRADPSFPIITGEVYTPG
BBE      --MNSRSVFLVLALSFCVSFGALSSIFDVTSTSEDFITCLQSNNSNVTITSQLVFTPA
          .      * ! *      . .      . . ! * *      . .      . .

P30986  DSDFNRFHLHSIQNPLFQNSLISKPSAIIILPGSKEELSNTIRCIRKGSWTIRLSGGHSY
P93479  NSDYFKLLHASMQNPLFAKPTVSKPSFIVMPGSKEELSSTVHCCTRESWTIRLSGGHSY
Sunf-19 NSSFPTVLQNYIRNLRFNETTTPKPFLIITAETHVSHIQAAVVCQKQNRLLLKTRSGGHDY
Sunf-15 NSSFPTVLQNYIRNLRFNETTTPKPFLIITAETHVSHIQAAVVCQKQNRLLLKTRSGGHDY
BBE      NTSYIPIWQAAADPIRFNKSYPKPSVIVPTDETIQTALLCAKKHGYEFIRIDGGHDF
          ! ! . .      * ! . * * ! *      . .      . . ! ! * !      ! ! * * * !

P30986  EGLSYTSDT--PFILIDLMLNLRVSIIDLESETAWVESGSTLGELYAITESSKLGFTAG
P93479  EGLSYTADT--PFVIVDMMLNLRISIDVLSETAWVESGATLGELYAIAQSDTLTGFTAG
Sunf-19 EGLSYLTNTNQPFIVDMFNLRINVDIEQETAWVQAGATLGEVYYIAEKSNNKHGFPAG
Sunf-15 EGLSYLTNTNQPFIVDMFNLRINVDIEQETAWVQAGATLGEVYYIAEKSNNKHGFPAG
BBE      EGNYSYTANA--PFVMLDLNMRATIEINVENRTALVQGGALLGELYTTISQKTDLTLYFAG
          * * * ! ! * * ! ! * ! * ! . . ! ! * * ! * * ! * ! * ! . . * *

P30986  WCPTVGTFGGISGGGFGMMSRKYGLAADNVVDAILIDANGAILDRQAMGEDVFWAIRGGG
P93479  WCPTVGSGGHIISGGGFGMMSRKYGLAADNVVDAILIDSNAILDREKMGDDVFWAIRGGG
Sunf-19 VCPTVGVGGHFSGGGYGMLMRKYGLSDNIVDAQIIDVNGKLLDRKSMGEDLFWAITGGG
Sunf-15 VCPTVGVGGHFSGGGYGMLMRKYGLSDNIVDAQIIDVNGKLLDRKSMGEDLFWAITGGG
BBE      IWAGVGSVGLSGGGYGMLLRKYGLGADNVLDIRFMDVNGNLDKSMGEDLFWAIRGGG
          . *      * ! * * * ! * ! * * * ! * ! * ! * ! * ! * * * ! * *

P30986  GGWGAIIYAWKIKLLPVPEDVTFRVTKNVAIDEATSLHKWQFVAEELEED-----FT
P93479  GGWGAIIYAWKIKLLPVPEDLTFRVTKNKGIEDASSLLHKWQYVADELDED-----FT
Sunf-19 GVSFGVVLAYKIKLVRVPEVTVFTIER-REEQNLSIAERWVQVADKLDRLFL--RMT
Sunf-15 GVSFGVVLAYKIKLVRVPEVTVFTIER-REEQNLSIAERWVQVADKLDRLFL--RMT
BBE      ASSFGIVLQWKLNLVPPERVTLFSVSY-TLEQGATDIFHKYQYVLPKFDRLDIRVQLN
          . * !      * ! * ! * * * ! * ! *      . .      . . ! ! *      ! ! *      !

P30986  LSVLGGADE-KQVWLTMLGFHFGLKTVAKSTFDLLFPELGLVEEDYLEMSWGESFAYLAG
P93479  VSVLGGVNG-NDAWLMFLGLHLGRKDAAKTIIDKFPPELGLVDKEFQEMSWGESMAFLSG
Sunf-19 FSVINDTNGGKTVRATFPTLYLGNSRNLVTLLNKDFPELGLQESDCTEMSWVESVLYYTG
Sunf-15 FSVINDTNGGKTVRATFPTLYLGNSRNLVTLLNKDFPELGLQESDCTEMSWVESVLYYTG
BBE      TEYIGNTTQ-KTVRIILFHGIYQGNIDTLLPLLNSQFPELNVTVREVCQEVNMQTTLEFGG
          . . . .      . .      . . ! *      . .      * * * . .      . .      . . *

P30986  LETVSQLNNRFLKFDERA--FKTKVDLTKEPLPSKAFYGLLERLSKEPN-GFIALNGFGG
P93479  LDTISELNNRFLKFDERA--FKTKVDFTKVSPLNVFRHALEMLSEQPG-GFIALNGFGG
Sunf-19 FPSGTPTTALLSRTQRLNPFKIKSDYVQNPISKQFQEFIFERMKELEN-QMLAFNPYGG
Sunf-15 FPSGTPTTALLSRTQRLNPFKIKSDYVQNPISKQFQEFIFERLKELEN-QMLAFNPYGG
BBE      FNISTPTSVLANRSAIPKLSFKGKSDYVQNPISPSGLRKLWRKMFENDNSQTLFMYTFGG
          . . .      . .      * * * . .      . .      . .      . .      . . *
  
```

FIG. 3A.

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```
P30986 QMSKISSDFTPFPHRSGTRLMEYIIVAWNQSEQKK---KTEFLDWLEKVYEFMKPFVSKN
P93479 KMSEISTDFTPFPHRKGTKLMFEYIIAWNQDEESK---IGEFSEWLAKFYDYLEPFVSKE
Sunf-19 RMSEISEFAKPFPHRSGNIAKIQYEVNWEDLSDEA---ENRYLNFTRLMYDYMTPFVSKN
Sunf-15 RMSEISEFAKPFPHRSGNIAKIQYEVNWEDLSDEA---ENRYLNFTRLMYDYMTPFVSKN
BBE KMEEYSDTAIPYPHRAGVLYQVFKRVDFVDQPSDKTLISLRRLAWLSFDKTLEPYVTSN
      !*!* *!*!* * , ! ! ! , ! , , !*!*!*

P30986 PRLGYVNHIDLDLGGIDWGNKTVVNNATIEISRSWGESYF-LSNYERLIRAKTLIDPNNVF
P93479 PRVGYVNHIDLDIGGIDWRNKSSTTNAVEIARNWGERYF-SSNYERLVKAKTLIDPNNVF
Sunf-19 PREAFLNYRDLDIG-INSHGR----NAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFF
Sunf-15 PRKAFLNYRDLDIG-INSHGR----NAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFF
BBE PREAYMNYNDLDLG--FDS-----AAYEEASEWGERYWKRENFKKLIRIKAKVDPENFF
      ** , !*!* **!* * * , !*.* * !*!*!* *!*!*!*

P30986 NHPQSIPPMANFD--YLEKTLGSDGGEVVI
P93479 NGPQSIPPMMKFEEIYMLKEL-----
Sunf-19 RNEQSIPTLSS-----
Sunf-15 RNEQSIPTLSS-----
BBE RHPQSIIPVFSRPLSDM-----
      , ! **** !
```

FIG. 3B.

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CLUSTAL W (1.7) multiple sequence alignment

```

P30230   MAKFASIIVLLFVALVVF AAFEPTMVEAQKLCQRPSGTWSGVCGNNNACKNQCIRLEKA
P30231   -----QKLCERPSGTWSGVCGNNNACKNQCINLEKA
P30224   MAKSATIVTLFFAALVFFAAL EAPMVVEAQKLCERPSGTWSGVCGNSNACKNQCINLEKA
defensin MAKISVAFNAFLLLLFVLAISEIGSVKG--ELCEKASQTWSGTCGKTKHCDDQCKSWEGA
Q01784   MEKKSALAALSFLLLLVLFVAQEIVVTEA--NTCEHLADTYRGVCFTNASCDDHCKNKAHL
                                     !*!! !*!*.*. . *.!.*

P30230   RHGSCNYVFPAHKCICYFPC-----
P30231   RHGSCNYVFPAHKCICYFPC-----
P30224   RHGSCNYVFPAHKCICYFPC-----
defensin AHGACHVRDGHMCF CYFNCSKAQKLAQDKLRAEELAKEKIEPEKATAKP
Q01784   ISGTCHD----WKCFCTQNC-----
               *!*!      *!*  *
```

FIG. 4.